IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: He et al.	Attorney Docket No.: PF140C2
Application Serial No.: Unassigned	Art Unit: Unassigned
Filed: Herewith	Examiner: Unassigned
Title: Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease-3 and 4	

SUBMISSION OF SUBSTITUTE/FORMAL DRAWINGS

Commissioner for Patents
Washington, D.C. 20231

Sir:

Please substitute the attached 7 sheets of formal drawings depicting Figures 1A-B, 2A-B, and 3A-C for the corresponding drawings of Figures 1-3 originally filed with the application. Included herewith, as required under 37 C.F.R. § 1.121(a)(3)(ii), is a copy of the figures as originally filed with changes marked. Acknowledgement of the receipt, approval, and entry of these formal drawings into the above captioned application is respectfully requested.

No fee is believed due for this submission. In the event that a fee is required in connection with this submission, please charge the required fee to Deposit Account No. 08-3425.

Respectfully submitted,

Dated: July 2, 2001

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JLK/LT/ba

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  1  GCACGAGAAACTTTGCTGTGCGCGTTCTCCCGCGCGCGGGCTCAACTTTGTAGAGCGAGG   60


 61  GGCCAACTTGGCAGAGCGCGCGGCCAGCTTTGCAGAGAGCGCCCTCCAGGGACTATGCGT  120


121  GCGGGGACACGGGTCGCTTTGGGCTCTTCCACCCCTGCGGAGCGCACTACCCCGAGCCAG  180


181  GGGCGGTGCAAGCCCCGCCCGGCCCTACCCAGGGCGGCTCCTCCCTCCGCAGCGCCGAGA  240


241  CTTTTAGTTTCGCTTTCGCTAAAGGGGCCCCAGACCCTTGCTGCGGAGCGACGGAGAGAG  300


301  ACTGTGCCAGTCCCAGCCGCCCTACCGCCGTGGGAACGATGGCAGATGATCAGGGCTGTA  360
  1                                       M  A  D  D  Q  G  C  I     8


361  TTGAAGAGCAGGGGGTTGAGGATTCAGCAAATGAAGATTCAGTGGATGCTAAGCCAGACC  420
  9   E  E  Q  G  V  E  D  S  A  N  E  D  S  V  D  A  K  P  D  R    28


421  GGTCCTCGTTTGTACCGTCCCTCTTCAGTAAGAAGAAGAAAAATGTCACCATGCGATCCA  480
 29   S  S  F  V  P  S  L  F  S  K  K  K  K  N  V  T  M  R  S  I    48


481  TCAAGACCACCCGGGACCGAGTGCCTACATATCAGTACAACATGAATTTTGAAAAGCTGG  540
 49   K  T  T  R  D  R  V  P  T  Y  Q  Y  N  M  N  F  E  K  L  G    68


541  GCAAATGCATCATAATAAACAACAAGAACTTTGATAAAGTGACAGGTATGGGCGTTCGAA  600
 69   K  C  I  I  I  N  N  K  N  F  D  K  V  T  G  M  G  V  R  N    88


601  ACGGAACAGACAAAGATGCCGAGGCGCTCTTCAAGTGCTTCCGAAGCCTGGGTTTTGACG  660
 89   G  T  D  K  D  A  E  A  L  F  K  C  F  R  S  L  G  F  D  V   108


661  TGATTGTCTATAATGACTGCTCTTGTGCCAAGATGCAAGATCTGCTTAAAAAAGCTTCTG  720
109   I  V  Y  N  D  C  S  C  A  K  M  Q  D  L  L  K  K  A  S  E   128


721  AAGAGGACCATACAAATGCCGCCTGCTTCGCCTGCATCCTCTTAAGCCATGGAGAAGAAA  780
129   E  D  H  T  N  A  A  C  F  A  C  I  L  L  S  H  G  E  E  N   148


781  ATGTAATTTATGGGAAAGATGGTGTCACACCAATAAAGGATTTGACAGCCCACTTTAGGG  840
149   V  I  Y  G  K  D  G  V  T  P  I  K  D  L  T  A  H  F  R  G   168


841  GGGATAGATGCAAAACCCTTTTAGAGAAACCCAAACTCTTCTTCATTCAGGCTTGCCGAG  900
169   D  R  C  K  T  L  L  E  K  P  K  L  F  F  I  Q  A  C  R  G   188


901  GGACCGAGCTTGATGATGCCATCCAGGCCGACTCGGGGCCCATCAATGACACAGATGCTA  960
189   T  E  L  D  D  A  I  Q  A  D  S  G  P  I  N  D  T  D  A  N   208
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 961  ATCCTCGATACAAGATCCCAGTGGAAGCTGACTTCCTCTTCGCCTATTCCACGGTTCCAG  1020
 209    P   R   Y   K   I   P   V   E   A   D   F   L   F   A   Y   S   T   V   P   G   228


1021  GCTATTACTCGTGGAGGAGCCCAGGAAGAGGCTCCTGGTTTGTGCAAGCCCTCTGCTCCA  1080
 229    Y   Y   S   W   R   S   P   G   R   G   S   W   F   V   Q   A   L   C   S   I   248


1081  TCCTGGAGGAGCACGGAAAAGACCTGGAAATCATGCAGATCCTCACCAGGGTGAATGACA  1140
 249    L   E   E   H   G   K   D   L   E   I   M   Q   I   L   T   R   V   N   D   R   268


1141  GAGTTGCCAGGCACTTTGAGTCTCAGTCTGATGACCCACACTTCCATGAGAAGAAGCAGA  1200
 269    V   A   R   H   F   E   S   Q   S   D   D   P   H   F   H   E   K   K   Q   I   288


1201  TCCCCTGTGTGGTCTCCATGCTCACCAAGGAACTCTACTTCAGTCAATAGCCATATCAGG  1260
 289    P   C   V   V   S   M   L   T   K   E   L   Y   F   S   Q                       303


1261  GGTACATTCTAGCTGAGAAGCAATGGGTCACTCATTAATGAATCACATTTTTTATGCTC  1320


1321  TTGAAATATTCAGAAATTCTCCAGGATTTTAATTTCAGGAAAATGTATT  1369
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  1 GCACGAGCGGATGGGTGCTATTGTGAGGCGGTTGTAGAAGAGTTTCGTGAGTGCTCGCAG 60

 61 CTCATACCTGTGGCTGTGTATCCGTGGCCACAGCTGGTTGGCGTCGCCTTGAAATCCCAG 120

121 GCCGTGAGGAGTTAGCGAGCCCTGCTCACACTCGGCGCTCTGGTTTTCGGTGGGTGTGCC 180

181 CTGCACCTGCCTCTTCCCGCATTCTCATTAATAAAGGTATCCATGGAGAACACTGAAAAC 240
  1                                             M  E  N  T  E  N  6

241 TCAGTGGATTCAAAATCCATTAAAAATTTGGAACCAAAGATCATACATGGAAGCGAATCA 300
  7  S  V  D  S  K  S  I  K  N  L  E  P  K  I  I  H  G  S  E  S  26

301 ATGGACTCTGGAATATCCCTGGACAACAGTTATAAATGGATTATCCTGAGATGGGTTTA 360
 27  M  D  S  G  I  S  L  D  N  S  Y  K  M  D  Y  P  E  M  G  L  46

361 TGTATAATAATTAATAATAAGAATTTTCATAAAAGCACTGGAATGACATCTCGGTCTGGT 420
 47  C  I  I  I  N  N  K  N  F  H  K  S  T  G  M  T  S  R  S  G  66

421 ACAGATGTCGATGCAGCAAACCTCAGGGAAACATTCAGAAACTTGAAATATGAAGTCAGG 480
 67  T  D  V  D  A  A  N  L  R  E  T  F  R  N  L  K  Y  E  V  R  86

481 AATAAAAATGATCTTACACGTGAAGAAATTGTGGAATTGATGCGTGATGTTCTAAAGAA 540
 87  N  K  N  D  L  T  R  E  E  I  V  E  L  M  R  D  V  S  K  E  106

541 GATCACAGCAAAAGGAGCAGTTTTGTTTGTGTGCTTCTGAGCCATGGTGAAGAAGGAATA 600
107  D  H  S  K  R  S  S  F  V  C  V  L  L  S  H  G  E  E  G  I  126

601 ATTTTTGGAACAAATGGACCTGTTGACCTGAAAAAAATAACAAACTTTTTCAGAGGGGAT 660
127  I  F  G  T  N  G  P  V  D  L  K  K  I  T  N  F  F  R  G  D  146

661 CGTTGTAGAAGTCTAACTGGAAAACCCAAACTTTTCATTATTCAGGCCTGCCGTGGTACA 720
147  R  C  R  S  L  T  G  K  P  K  L  F  I  I  Q  A  C  R  G  T  166

721 GAACTGGACTGTGGCATTGAGACAGACAGTGGTGTTGATGATGACATGGCCGTGTCATAAA 780
167  E  L  D  C  G  I  E  T  D  S  G  V  D  D  D  M  A  C  H  K  186

781 ATACCAGTGGAGGCCGACTTCTTGTATGCATACTCCACAGCCACCTGGTTATTATTCTTGG 840
187  I  P  V  E  A  D  F  L  Y  A  Y  S  T  A  P  G  Y  Y  S  W  206
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```
841  CGAAATTCAAAGGATGGCTCCTGGTTCATCCAGTCGCTTTGTGCCATGCTGAAACAGTAT  900
207   R   N   S   K   D   G   S   W   F   I   Q   S   L   C   A   M   L   K   Q   Y  226


901  GCCGACAAGCTTGAATTTATGCACATTCTTACCCGGGTTAACCGAAAGGTGGCAACAGAA  960
227   A   D   K   L   E   F   M   H   I   L   T   R   V   N   R   K   V   A   T   E  246


961  TTTGAGTCCTTTTCCTTTGACGCTACTTTTCATGCAAAGAAACAGATTCCATGTATTGTT  1020
247   F   E   S   F   S   F   D   A   T   F   H   A   K   K   Q   I   P   C   I   V  266


1021 TCCATGCTCACAAAAGAACTCTATTTTTATCACTAAAGAAATGGTTGGTTGGTGGTTTTT  1080
267   S   M   L   T   K   E   L   Y   F   Y   H   *                               277


1081 TTTAGTTTGTATGCCAAGTGAGAAGATGGTATATTTGGGTACTGTATTTCCCTCTCATTG  1140


1141 GGGACCTACTCTCATGCTG  1159
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FIGURE 3A

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                         10              20              30         40
1   M A D D - - - - Q - - - - - - - - - - - - - - - - - - - - - - - - - G C I E E Q G V E   ICE-LAP-3
1   M E N T - - - E - - - - - - - - - - - - - - - - - - - - - - N S V D S K S I K N         ICE-LAP-4
1   M A D K V L K E K R K L F I R S M - - - G E G T I N G L L D E L L Q T R V L N           Human ICE
1   M M R Q - - D R R S L L E R N I M P S S H L K V D E I L E V L I A R Q V L N             CBD-3

                         50              60              70         80
16  S A N E D S V D A - - - - - - - - - - - - - - - - K P D R S S F                         ICE-LAP-3
16  - - - - L E P - - - - - - - - - - - - - - - - K I I H G E -                             ICE-LAP-4
37  K E E M E K V K R E N A T V M D K T R A L I D S V -                                     Human ICE
38  S D N G D M I N S - C G T V R E K R R E I V K A V Q R R G D V A F D A F Y D A L         CBD-3

                         90              100             110        120
32  - - - - V P S L F S K K K K N V T M R S I -                                             ICE-LAP-3
25  - - - E S M D S G I S L D N S -                                                         ICE-LAP-4
62  - - - I P K G A Q A C Q I C I T Y I C -                                                 Human ICE
77  R S T G H E G L A E V L E P L A R S V D S N A V E F E Q P M S P A S H R R S R A         CBD-3

                         130             140             150        160
49  - - - K T T R D R U P T - -                                                            ICE-LAP-3
37  - E E D S V L A G T L G - L S A D T S G N Y -                                           ICE-LAP-4
78  L S P A G Y T S P T R V H R D S V S S V S S F T S V Q D I Y S R A R S R S R S R         Human ICE
117                                                                                        CBD-3

                         170             180             190        200
58  - I N M Q S Q G - - - - V L S S F F A P Q A V Q D N P - -                               ICE-LAP-3
37                                                                                          ICE-LAP-4
99  A H S S D R H N Y S S P P V N A E D S Q P S S A N S S F T G C S S L G Y S S S           Human ICE
157                                                                                        CBD-3
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FIGURE 3B

FIGURE 3C

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                    410                 420                 430        440
204  - - - - D T D A N P R Y - - - - - - - - - - - - - - - - K I P V E A D F L   F A Y S T   ICE-LAP-3
181  - - - - D M A C H - - - - - - - - - - - - - - - - - - - K I P V E A D F L   Y A Y S T   ICE-LAP-4
307  - - - - L P T T E E - F E - - - - - - - - - D D A I K    K A H I V E A D F L A P C S S   Human ICE
382  R G W D N R D G F L F N F L G C V R P Q V Q Q V W R      K K F S Q A D I L I A Y A T     CBD-3

                    450                 460                 470        480
226  V P G V Y S W R S P G R I G S W R V Q A I C S T L E B H G K D L E I M Q I L T R V    ICE-LAP-3
200  A P G V Y S W R N S - K D G S W F I Q S L C A M L K Q Y A D K L E F M H I L T R V    ICE-LAP-4
334  T P D N V S W R N S H P T M G S V F I G R L I E H M Q E Y A C S C D V E E I F       Human ICE
422  T A Q X V S M R N S - A R G S W F I Q A V C E V F S T H A K D M D V V E L L T E V   CBD-3

                    490                 500                 510        520
266  N D R V A R H F E S Q S D D P H F H E K K Q I P C V V S M L T K E L V F - - - - -   ICE-LAP-3
240  N R K V A T E F E S F S F D A T F H A K K Q I P C I V S M L T K E L V F - - - - -   ICE-LAP-4
371  N K K V A R F S F E Q P D G R A Q M P T T E R V T - - - L T R C F Y L F P G H      Human ICE
462  N K K V A C G F Q T S Q G S N I L - - - K Q M P E M T S R E L K K F V F W P E A    CBD-3

302  - - S L O .                                                                         ICE-LAP-3
276  - - Y H .                                                                           ICE-LAP-4
404  R N S A V                                                                           Human ICE
499                                                                                      CBD-3
```

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

```
1        GCACGAGAAACTTTGCTGTGCGCGTTCTCCCGCGCGCGGGCTCAACTTTGTAGAGCGAGG

61       GGCCAACTTGGCAGAGCGCGCGGCCAGCTTTGCAGAGAGCGCCCTCCAGGGACTATGCGT
1                                                            M   R
121      GCGGGGACACGGGTCGCTTTGGGCTCTTCCACCCCTGCGGAGCGCACTACCCCGAGCCAG
3        A   G   T   R   V   A   L   G   S   S   T   P   A   E   R   T   T   P   S   Q
181      GGGCGGTGCAAGCCCCGCCCGGCCCTACCCAGGGCGGCTCCTCCCTCCGCAGCGCCGAGA
23       G   R   C   K   P   R   P   A   L   P   R   A   A   P   P   S   A   A   P   R
241      CTTTTAGTTTCGCTTTCGCTAAAGGGGCCCCAGACCCTTGCTGCGGAGCGACGGAGAGAG
43       L   L   V   S   L   S   L   K   G   P   Q   T   L   A   A   E   R   R   R   E
301      ACTGTGCCAGTCCCAGCCGCCCTACCGCCGTGGGAACGATGGCAGATGATTCAGGGCTGT
63       T   V   P   V   P   A   A   L   P   P   W   E   R   W   Q   M   I   Q   G   C
361      ATTGAAGAGCAGGGGGTTGAGGATTCAGCAAATGAAGATTCAGTGGATGCTAAGCCAGAC
83       I   E   E   Q   G   V   E   D   S   A   N   E   D   S   V   D   A   K   P   D
421      CGGTCCTCGTTTGTACCGTCCCTCTTCAGTAAGAAGAAGAAAAATGTCACCATGCGATCC
103      R   S   S   F   V   P   S   L   F   S   K   K   K   K   N   V   T   M   R   S
481      ATCAAGACCACCCGGGACCGAGTGCCTACATATCAGTACAACATGAATTTTGAAAAGCTG
123      I   K   T   T   R   D   R   V   P   T   Y   Q   Y   N   M   N   F   E   K   L
541      GGCAAATGCATCATAATAAACAACAAGAACTTTGATAAAGTGACAGGTATGGGCGTTCGA
143      G   K   C   I   I   I   N   N   K   N   F   D   K   V   T   G   M   G   V   R
601      AACGGAACAGACAAAGATGCCGAGGCGCTCTTCAAGTGCTTCCGAAGCCTGGGTTTTGAC
163      N   G   T   D   K   D   A   E   A   L   F   K   C   F   R   S   L   G   F   D
661      GTGATTGTCTATAATGACTGCTCTTGTGCCAAGATGCAAGATCTGCTTAAAAAAGCTTCT
183      V   I   V   Y   N   D   C   S   C   A   K   M   Q   D   L   L   K   K   A   S
721      GAAGAGGACCATACAAATGCCGCCTGCTTCGCCTGCATCCTCTTAAGCCATGGAGAAGAA
203      E   E   D   H   T   N   A   A   C   F   A   C   I   L   L   S   H   G   E   E
781      AATGTAATTTATGGGAAAGATGGTGTCACACCAATAAAGGATTTGACAGCCCACTTTAGG
223      N   V   I   Y   G   K   D   G   V   T   P   I   K   D   L   T   A   H   F   R
841      GGGGATAGATGCAAAACCCTTTTAGAGAAACCCAAACTCTTCTTCATTCAGGCTTGCCGA
243      G   D   R   C   K   T   L   L   E   K   P   K   L   F   F   I   Q   A   C   R
901      GGGACCGAGCTTGATGATGGCATCCAGGCCGACTCGGGGCCCATCAATGACACAGATGCT
263      G   T   E   L   D   D   G   I   Q   A   D   S   G   P   I   N   D   T   D   A
961      AATCCTCGATACAAGATCCCAGTGGAAGCTGACTTCCTCTTCGCCTATTCCACGGTTCCA
283      N   P   R   Y   K   I   P   V   E   A   D   F   L   F   A   Y   S   T   V   P
1021     GGCTATTACTCGTGGAGGAGCCCAGGAAGAGGCTCCTGGTTTGTGCAAGCCCTCTGCTCC
303      G   Y   Y   S   W   R   S   P   G   R   G   S   W   F   V   Q   A   L   C   S
1081     ATCCTGGAGGAGCACGGAAAAGACCTGGAAATCATGCAAATCCTCCACCAGGGTGAATGA
323      I   L   E   E   H   G   K   D   L   E   I   M   Q   I   L   H   Q   G   E   *
1141     CAGAGTTGCCAGGCACTTTGAGTCTCAGTCTGATGACCCACACTTCCATGAGAAGAAGCA

1201     GATCCCCTGTGTGGTCTCCATGCTCACCAAGGAACTCTACTTCAGTCAATAGCCATATCA

1261     GGGGTACATTCTAGCTGAGAAGCAATGGGTCACTCATTAATGAATCACATTTTTTTATGC

1321     TCTTGAAATATTCAGAAATTCTCCAGGATTTTAATTTCAGGAAAATGTATT
```

Figure 1

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1          GCACGAGCGGATGGGTGCTATTGTGAGGCGGTTGTAGAAGAGTTTCGTGAGTGCTCGCAG

61         CTCATACCTGTGGCTGTGTATCCGTGGCCACAGCTGGTTGGCGTCGCCTTGAAATCCCAG

121        GCCGTGAGGAGTTAGCGAGCCCTGCTCACACTCGGCGCTCTGGTTTTCGGTGGGTGTGCC

181        CTGCACCTGCCTCTTCCCGCATTCTCATTAATAAAGGTATCCATGGAGAACACTGAAAAC
1                                                     M  E  N  T  E  N

241        TCAGTGGATTCAAAATCCATTAAAAATTTGGAACCAAAGATCATACATGGAAGCGAATCA
7           S  V  D  S  K  S  I  K  N  L  E  P  K  I  I  H  G  S  E  S

301        ATGGACTCTGGAATATCCCTGGACAACAGTTATAAAATGGATTATCCTGAGATGGGTTTA
27          M  D  S  G  I  S  L  D  N  S  Y  K  M  D  Y  P  E  M  G  L

361        TGTATAATAATTAATAATAAGAATTTTCATAAAAGCACTGGAATGACATCTCGGTCTGGT
47          C  I  I  I  N  N  K  N  F  H  K  S  T  G  M  T  S  R  S  G

421        ACAGATGTGCTGATGCAGCAAACCTCAGGGAAACATTCAGAAACTTGAAATATGAAGTCAGG
67          T  D  V  D  A  A  N  L  R  E  T  F  R  N  L  K  Y  E  V  R

481        AATAAAAATGATCTTACACGTGAAGAAATTGTGGAATTGATGCGTGATGTTTCTAAAGAA
87          N  K  N  D  L  T  R  E  E  I  V  E  L  M  R  D  V  S  K  E

541        GATCACAGCAAAAGGAGCAGTTTTGTTTGTGTGCTTCTGAGCCATGGTGAAGAAGGAATA
107         D  H  S  K  R  S  S  F  V  C  V  L  L  S  H  G  E  E  G  I

601        ATTTTTGGAACAAATGGACCTGTTGACCTGAAAAAAATAACAAACTTTTTCAGAGGGGAT
127         I  F  G  T  N  G  P  V  D  L  K  K  I  T  N  F  F  R  G  D

661        CGTTGTAGAAGTCTAACTGGAAAACCCAAACTTTTCATTATTCAGGCCTGCCGTGGTACA
147         R  C  R  S  L  T  G  K  P  K  L  F  I  I  Q  A  C  R  G  T

721        GAACTGGACTGTGGCATTGAGACAGACAGTGGTGTTGATGATGACATGGCCGTGTCATAA
167         E  L  D  C  G  I  E  T  D  S  G  V  D  D  D  M  A  C  H  K

781        ATACCAGTGGAGGCCGACTTCTTGTATGCATACTCCACAGCCACCTGGTTATTATTCTTGG
187         I  P  V  E  A  D  F  L  Y  A  Y  S  T  A  P  G  Y  Y  S  W

841        CGAAATTCAAAGGATGGCTCCTGGTTCATCCAGTCGACTCGCTTTGTGCCATGCTGAAACAGTAT
207         R  N  S  K  D  G  S  W  F  I  Q  S  L  C  A  M  L  K  Q  Y

901        GCCGACAAGCTTGAATTTATGCACATTCTTACCCGGGTTAACCGAAAGGTGGCAACAGAA
227         A  D  K  L  E  F  M  H  I  L  T  R  V  N  R  K  V  A  T  E

961        TTTGAGTCCTTTTCCTTTGACGCTACTTTTCATGCAAAGAAACAGATTCCATGTATTGTT
247         F  E  S  F  S  F  D  A  T  F  H  A  K  K  Q  I  P  C  I  V

1021       TCCATGCTCACAAAAGAACTCTATTTTTATCACTAAAGAAATGGTTGGTTGGTGGTTTTT
267         S  M  L  T  K  E  L  Y  F  Y  H  *

1081       TTTAGTTTGTATGCCAAGTGAGAAGATGGTATATTTGGGTACTGTATTTCCCTCTCATTG

1141       GGGACCTACTCTCATGCTG
```

Figure 2

Figure 3